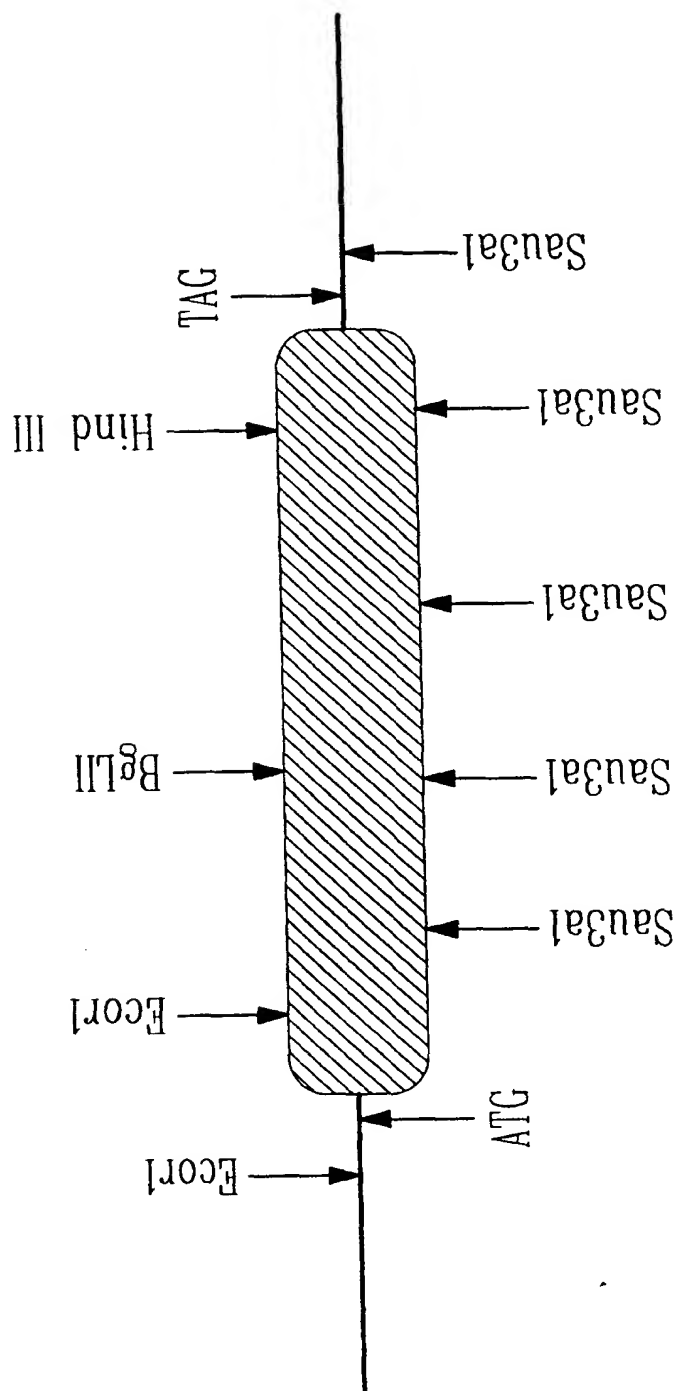


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FIG. 1A

Restriction map of the gene encoding for P-40



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1	agtgtgaaat	cttcagagaa	gaatttctct	ttagttcttt	gcaagaaagg	agagataaag
61	acactttttc	aaaaatggca	atggtatcag	aattcctcaa	gcaggcctgg	tttattgaaa
121	atgaagagca	ggaatatgtt	caaaactgtga	agtcataccaa	agggtgtccc	ggatcagcgg
181	tgagccctta	tcctaccttc	aatccatcct	cggatgtcgc	tgccttgcct	aaggccataa
241	tgggtaaaagg	tgtggatgaa	gcaaccatca	ttgacattct	aactaagcga	aacaatgcac
301	agcgtcaaca	gatcaaaagca	gcataatctcc	aggaaacacagg	aaagccctcg	gatgaaacac
361	ttaagaaaagc	ccttacaggt	caccttgagg	aggttgtttt	agctctgcta	aaaactccag
421	cgcaatttga	tgctgatgaa	cttcgtgctg	ccatgaaagg	ccttggaact	gatgaagata
481	ctctaattga	gattttggca	tcaagaaacta	acaaaagaaat	cagagacatt	aacaggggtct
541	acagagagga	actgaagaga	gacttgcca	aagacataac	ctcagacaca	tctggagatt
601	ttcggaacgc	tttgctttct	cttgctaagg	gtgaccgatac	tgaggacttt	ggtgtgaatg
661	aagacttggc	tgatttcagat	gccagggcct	tgtatgaagc	aggagaaaag	agaaaagggga

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721	cagacgtaaa	cgtgttcaat	accatcctta	ccaccagaag	ctatccacaa	cttcgcagag
781	tgtttcagaa	atacaccaag	tacagtaagc	atgacatgaa	caaagtcttg	gacctggagt
841	tgaaaaggta	cattgagaaa	tgcctcacag	ctatcgtgaa	gtcgcgcaca	agcaaacccag
901	ctttctttgc	agagaagcct	catcaagcca	tgaaaagggt	tggaaactgc	cataaggcat
961	tgatcaggat	tatggtttcc	cgttctgaaa	ttgacatgaa	tgatatcaaa	gcattctcttc
1021	agaagatgta	tggatatctcc	ctttgccaaag	ccatcctgga	tgaaacccaaa	ggagatttatg
1081	agaaaaatcct	ggtggctctt	tgtggaggaa	actaaacatt	cccttgatgg	tctcaagcta
1141	tgatcagaaag	actttaatta	tatatatttca	tcctataagc	ttaaatagga	aagtttcttc
1201	aacaggatta	cagtgtagct	acctacatgc	tgaaaaaatat	agccttttaa	tcattttttat
1261	attataactc	tgtataatag	agataagtcc	attttttaa	aatgttttcc	ccaaaccata
1321	aaaccctata	caagttgttc	tagtaacaat	acatgagaaa	gatgtctatg	tagctgaaaa
1381	baaaatgacg	tcacaagac				

11

77-111

[illegible]

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MAMVSEFLKQAWFIENEEQEVVQTVKSSKGGPGSAVSPYPTFFNPSSDVAALHKAIMVK
GVDEATIIDILTKRNNAQRQOIKAAYLQETGKPLDETLLKKALTGHLEEVVLALLKTPA
QFDADDELRAAMKGLGTDEDTLIEILLASRTNKEIRDINRVYREELKRD LAKDITSDTSG
DFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKGTDVNVFNTILTTTRSYPO
LRRVFQKYTKYSKHD MNKVLDLELKGDI EKCLTAIVKCATSKPAFFAEKLHQAMKGVG
TRHKALIRIMVSRSEIDMNDIKAFYQKMYGISLQCQAILDET KGDYEKILVALCGGN

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10 20 30 40 50 60
* * * * *
3' GTAGCGACCGGCTCAGCTGGAATTCGGCGCGCTCGATTTTGTGCTGTGACGTCATTTATT
5' CATCGCTGGCCGCGAGTCGACCTTAAGCGCGCGCAGCTAAAAACAGAACACTGCAGTAAATAA
A T G A Q L E F A A A S I F L S C D V I L F>
* R P A L S W N S R P R F F C L V T S F Y>
S D R R S A G I R G R V D F F V L * R H F I>
<Y R G A S L Q F E R G R R N K Q R T V D N * K
<A V P A * S S N A A A D I K K D Q S T M K N
<L S R R E A P I R P R T S K K T K H R * K I

70 80 90 100 110 120 130
* * * * *
TTCAGCTACATAGACATCTTCTCATGTTACTAGAACAACTGTATAGGGTTTATGGTTGGGAAA
AAGTCGATGTATCTGTAGAAAGAGTACAATGATCTTGTGAACATATCCCAAAATACCAACCCCTTT
S A T * T S F S C Y * N N L Y R V L W F G E>
F Q L H R H L S H V T R T T C I G F Y G L G K>
F S Y I D I F L M L L E Q L V * G F M V W G K>
<* S C L C R E * T V L V V Q I P N * P K P F
<E A V Y V D K E H * * F L K Y L T K H N P S F
<K L * M S M K R M N S S C S T Y P K I T Q P F

FILE

140	150	160	170	180	190	200
*	*	*	*	*	*	*
ACATTTTAAAAATGGACTTATCTCTATTTATACAGAGTTAATAATAAAAAATGATTATAAAGGCTATA						
TGTAAAAAATTTTTTACCTGAATAGAGATAAATATGTCTCAATATTATATTTTACTAAATTTCCGATAT						
N I F K K W T Y L Y Y T E L * Y K N D L K A I>						
T F L K K N G L I S I I Q S Y N I K M I * R L Y>						
H F * K M D L S L L Y R V I I * K * F K G Y>						
<V N K F F P S I E I I C L * L I F I I * L S Y						
<M K L F H V * R * * V S N Y Y L F S K F A I						
<C K * F I S K D R N Y L T I I Y F H N L P * I						

210	220	230	240	250	260	270
*	*	*	*	*	*	*
TTTTTCAGCATG	TTAGCTACACT	GTAAATCCTG	TGTTGAAGAA	AACTTTCCTAT	TTTAAGCTTAT	AGGAT
AAAAAGTCGTAC	ATCCATCGATG	ACATTAGGACA	CACTTCTTTGA	AAAGGATAAA	TTCGAATATC	CTA
F F S M *	V A T L *	S C *	R N F P	I * A Y R	M>	
F, S A C R *	L H C N P	V E E T F	L F K L I	G>		
I F Q H V G S	Y T V I L L	K K L S Y	L S L *	D>		
<K E A H L Y	S C Q L G T	S S V K R N	L S I P	H		
<N K L M Y T	A V S Y D Q	Q L F K G I	* A * L I			
<K * C T P L	* V T I R N	F F S E *	K L K Y S			

FIRST

[illegible]

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[illegible]

350	360	370	380	390	400
*	*	*	*	*	*
AAAGAGCCACGAGATTTTCTCATAATCTCCTTTGGTTTCATCCAGATGGCTTGGCAAGGAGATA					
TTTCTCGGTGTCCTAAAGAGTATTAGAGGAACCAAGTAGGTCCTACCGAACCGTTTCCCTCTAT					
Q R A T R I F S * S P L V S S R M A W Q R E I >					
K E P P G F S H N L L W F H P G W L G K G R Y >					
K' S H Q D F L I I S F G F I Q D G L A K G D >					
<L S G G P N E * L R R Q N * G P H S P L P L Y					
<u><L A V L I K E Y D G K T E D L I A Q C L S I</u>					
<F L W W S K R M I E K P K M W S P K A F P S V					

GT-III

Parameter	Unit	Value	Standard Error	t-value	p-value
β_0		1.0000	0.0000		
β_1		0.0000	0.0000		
β_2		0.0000	0.0000		
β_3		0.0000	0.0000		
β_4		0.0000	0.0000		
β_5		0.0000	0.0000		
β_6		0.0000	0.0000		
β_7		0.0000	0.0000		
β_8		0.0000	0.0000		
β_9		0.0000	0.0000		
β_{10}		0.0000	0.0000		
β_{11}		0.0000	0.0000		
β_{12}		0.0000	0.0000		
β_{13}		0.0000	0.0000		
β_{14}		0.0000	0.0000		
β_{15}		0.0000	0.0000		
β_{16}		0.0000	0.0000		
β_{17}		0.0000	0.0000		
β_{18}		0.0000	0.0000		
β_{19}		0.0000	0.0000		
β_{20}		0.0000	0.0000		
β_{21}		0.0000	0.0000		
β_{22}		0.0000	0.0000		
β_{23}		0.0000	0.0000		
β_{24}		0.0000	0.0000		
β_{25}		0.0000	0.0000		
β_{26}		0.0000	0.0000		
β_{27}		0.0000	0.0000		
β_{28}		0.0000	0.0000		
β_{29}		0.0000	0.0000		
β_{30}		0.0000	0.0000		
β_{31}		0.0000	0.0000		
β_{32}		0.0000	0.0000		
β_{33}		0.0000	0.0000		
β_{34}		0.0000	0.0000		
β_{35}		0.0000	0.0000		
β_{36}		0.0000	0.0000		
β_{37}		0.0000	0.0000		
β_{38}		0.0000	0.0000		
β_{39}		0.0000	0.0000		
β_{40}		0.0000	0.0000		
β_{41}		0.0000	0.0000		
β_{42}		0.0000	0.0000		
β_{43}		0.0000	0.0000		
β_{44}		0.0000	0.0000		
β_{45}		0.0000	0.0000		
β_{46}		0.0000	0.0000		
β_{47}		0.0000	0.0000		
β_{48}		0.0000	0.0000		
β_{49}		0.0000	0.0000		
β_{50}		0.0000	0.0000		
β_{51}		0.0000	0.0000		
β_{52}		0.0000	0.0000		
β_{53}		0.0000	0.0000		
β_{54}		0.0000	0.0000		
β_{55}		0.0000	0.0000		
β_{56}		0.0000	0.0000		
β_{57}		0.0000	0.0000		
β_{58}		0.0000	0.0000		
β_{59}		0.0000	0.0000		
β_{60}		0.0000	0.0000		
β_{61}		0.0000	0.0000		
β_{62}		0.0000	0.0000		
β_{63}		0.0000	0.0000		
β_{64}		0.0000	0.0000		
β_{65}		0.0000	0.0000		
β_{66}		0.0000	0.0000		
β_{67}					

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480	490	500	510	520	530	540
*	*	*	*	*	*	*
GATCAATGCCTTATTGCGAGTTC	AACACCTTTTCATGGCTTGATGAAGCTTCTCTGCAAAAGAAAGCT	5'				
CTAGTTACGGAATAACGCTCAAGGTTGTGGAAGTACCGAACTACTTCGAAGAGACGTTTCTTCGA	3'					
I N A L L R V P T P F M A * * S F S A K K A>						
* S M P Y C E F Q H L S W L D E A S L Q R K L>						
D Q C L I A S S N T F H G L M K L L C K E S X>						
<D I G * Q S N W C R E H S S S A E R C L F						
<I L A K N R T G V G K M A Q H L K E A F F A						
<S * H R I A L E L V K * P K I F S R Q L S L						

HL-III

[illegible]

Vector
p-40
p-40

CO
OL
ER
L

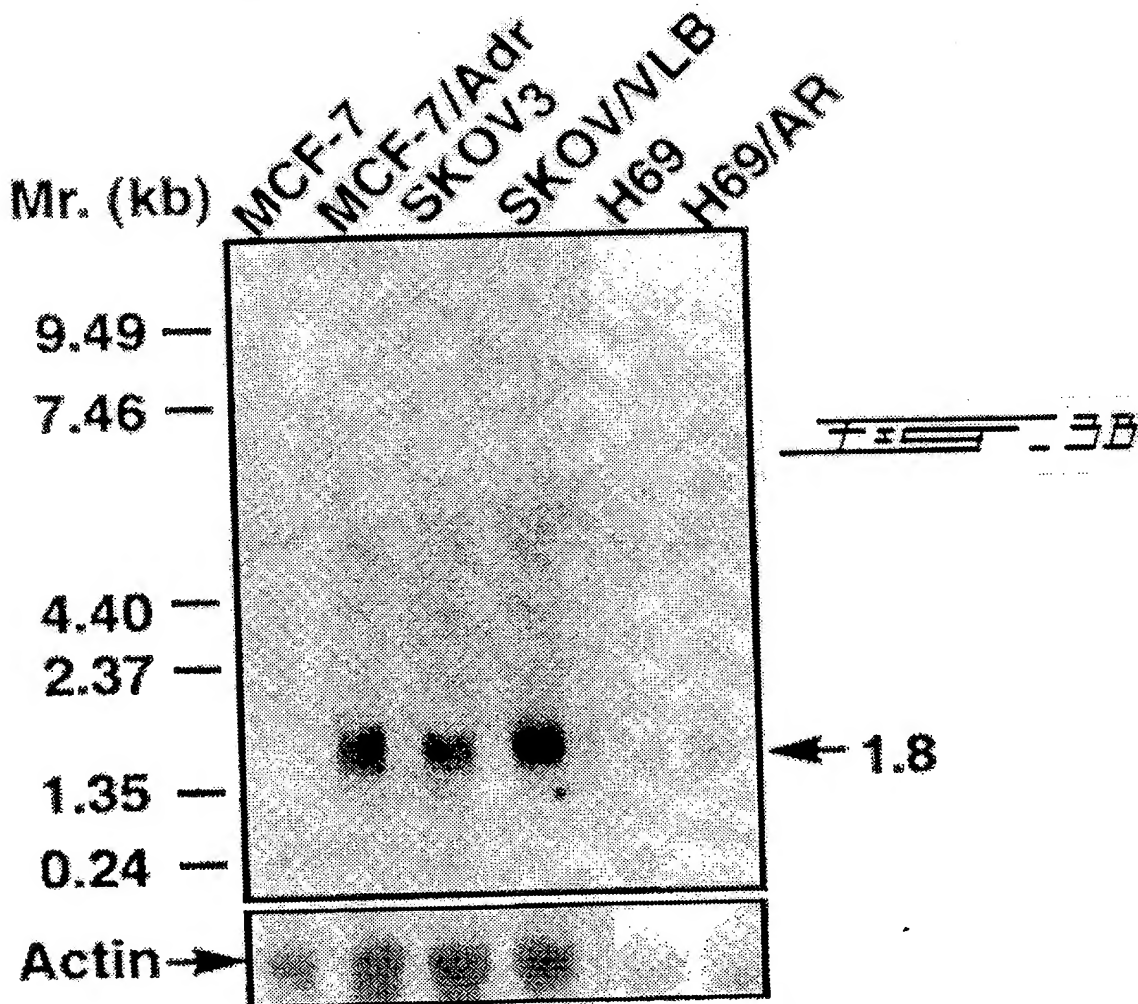
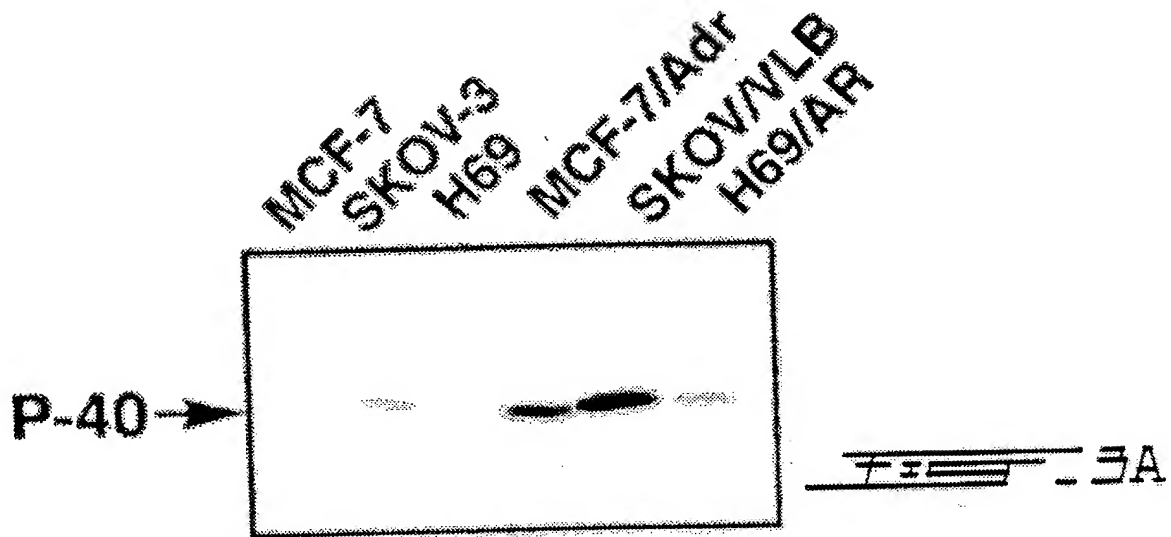
五三

PM96 9G2b

FEEL - VE

042

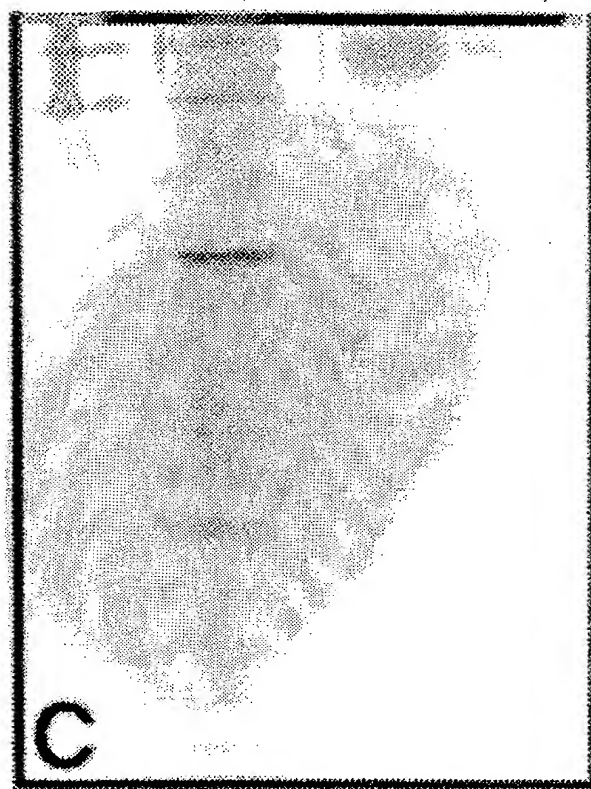
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IgG2b
IPM96
IgG2b
IPM96

P-40 →



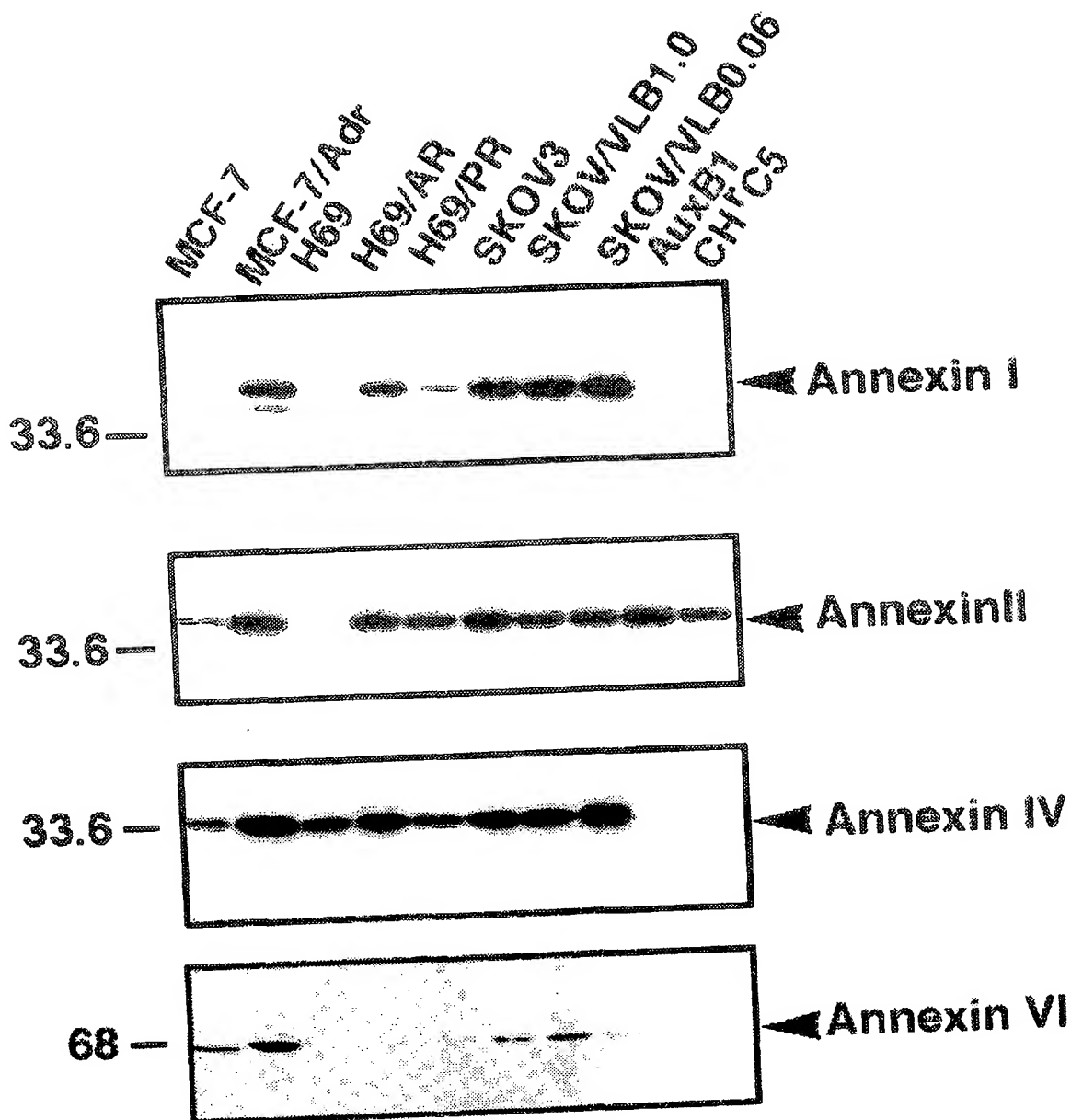
[³⁵S]Met

[³²Pi]

FIG. 4

000E20" 52662560

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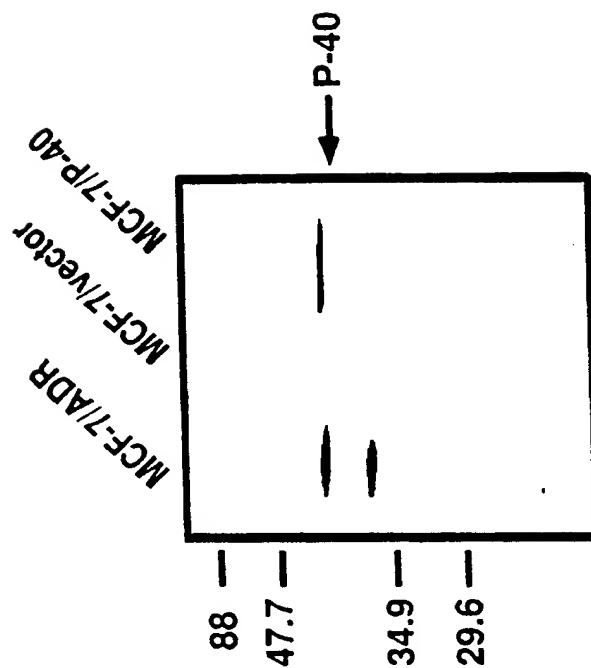
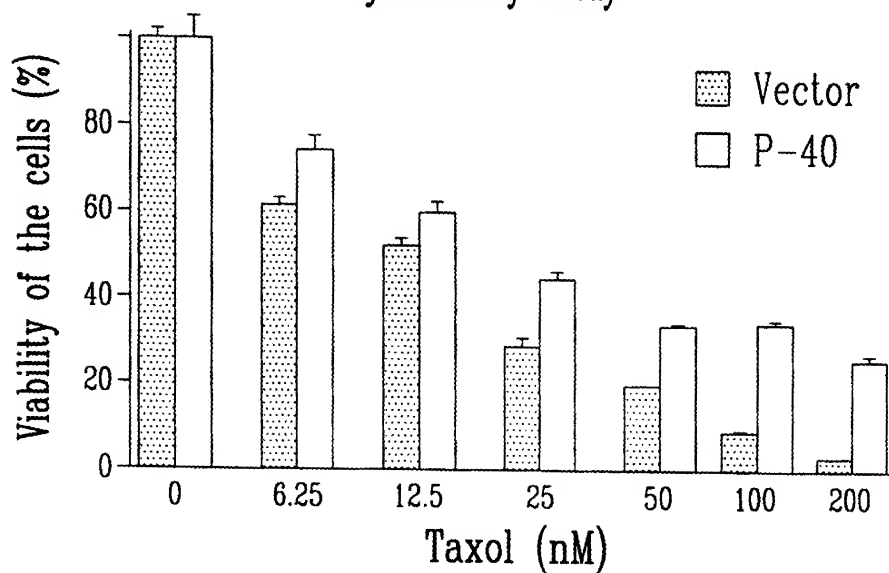


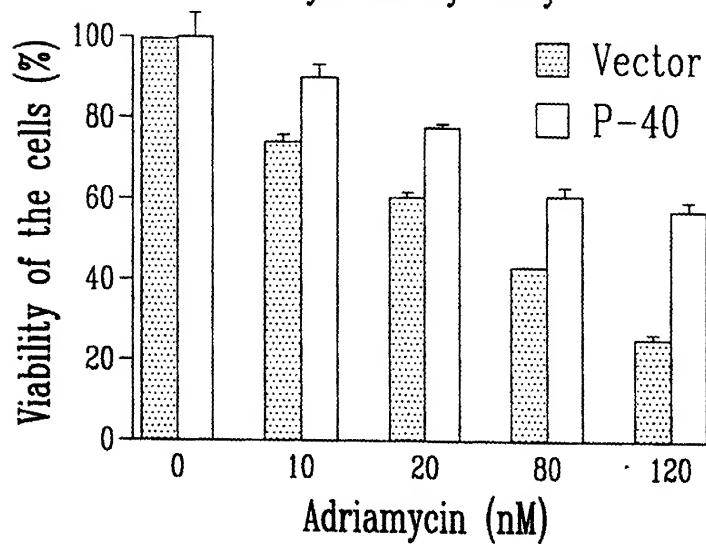
FIG. 6A

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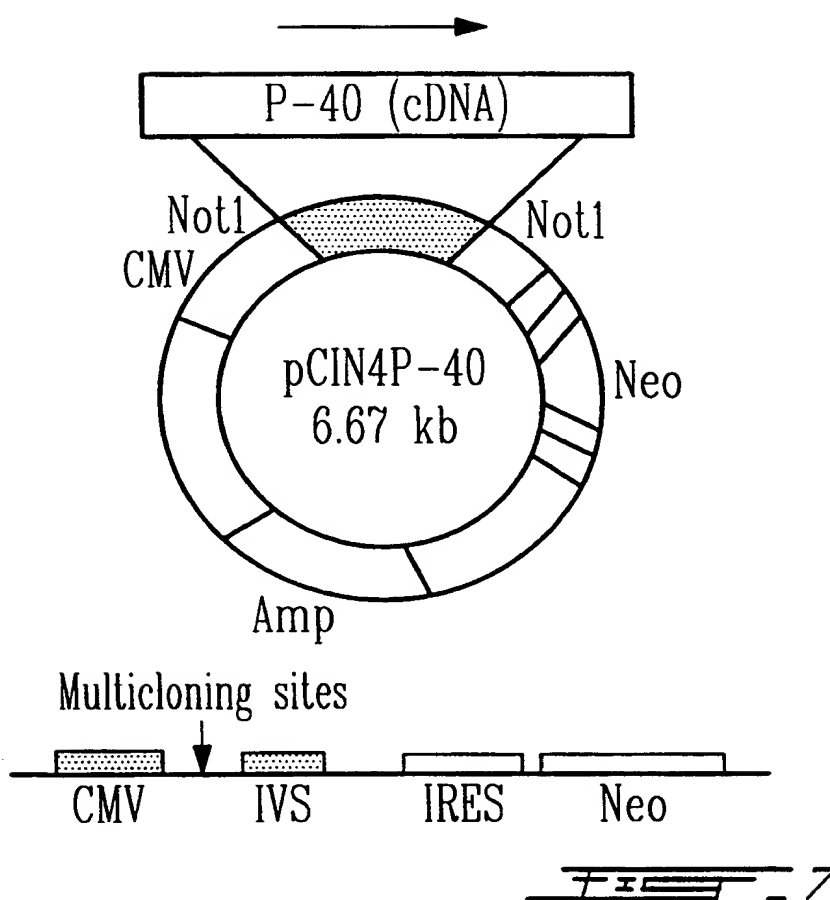
Cytotoxicity assay

FIG. 5B

Cytotoxicity assay

FIG. 5C

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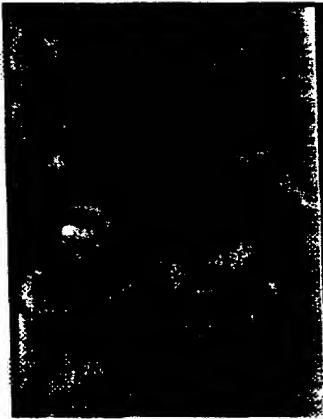


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MCF-7/Adr
(800X)



Vector-MCF-7
(600X)



P-40-MCF-7
(400X)



Fig. 1 - BB

Mr.(kDa) 1 2

109 —

78 —

46.7 —

34.5 —

26.8 —

20.5 —



←P-40

Fig. 2 - BA

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